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#2

RAW SEQUENCE LISTING DATE: 03/29/2001
 PATENT APPLICATION: US/09/782,714 TIME: 09:59:32

Input Set : N:\Crf3\RULE60\09782714.txt
 Output Set: N:\CRF3\03292001\I782714.raw

3 <110> APPLICANT: Darst, Seth A
 4 Zhang, Gongyi
 5 Campbell, Elizabeth
 6 Minakin, Leonid
 7 Severinov, Konstantin
 9 <120> TITLE OF INVENTION: A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE AND METHODS
 10 OF USE THEREOF
 12 <130> FILE REFERENCE: 600-1-258
 14 <140> CURRENT APPLICATION NUMBER: 09/782,714
 15 <141> CURRENT FILING DATE: 2001-02-13
 17 <150> PRIOR APPLICATION NUMBER: 09/396,651
 18 <151> PRIOR FILING DATE: 1999-09-15
 21 <160> NUMBER OF SEQ ID NOS: 4
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1525
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Thermus aquaticus
 30 <220> FEATURE:
 31 <221> NAME/KEY: SITE
 32 <222> LOCATION: (1247)
 33 <223> OTHER INFORMATION: Any amino acid can be at this position
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 37 1 5 10 15
 39 Lys Ile Arg Ser Trp Ser Tyr Gly Glu Val Glu Lys Pro Glu Thr Ile
 40 20 25 30
 42 Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Asp Glu Arg
 43 35 40 45
 45 Ile Phe Gly Pro Ile Lys Asp Tyr Glu Cys Ala Cys Gly Lys Tyr Lys
 46 50 55 60
 48 Arg Gln Arg Phe Glu Gly Lys Val Cys Glu Arg Cys Gly Val Glu Val
 49 65 70 75 80
 51 Thr Arg Ser Ile Val Arg Arg Tyr Arg Met Gly His Ile Glu Leu Ala
 52 85 90 95
 54 Thr Pro Ala Ala His Ile Trp Phe Val Lys Asp Val Pro Ser Lys Ile
 55 100 105 110
 57 Gly Thr Leu Leu Asp Leu Phe Ala Thr Glu Leu Glu Val Leu Tyr
 58 115 120 125
 60 Phe Asn Lys Tyr Ile Val Leu Asp Pro Lys Gly Ala Val Leu Asp Gly
 61 130 135 140
 63 Val Pro Val Glu Lys Arg Gln Leu Leu Thr Asp Glu Glu Tyr Arg Glu
 64 145 150 155 160
 66 Leu Arg Tyr Gly Lys Gln Glu Thr Tyr Pro Leu Pro Ala Gly Val Asp
 67 165 170 175
 69 Ala Leu Val Lys Asp Gly Glu Glu Val Val Lys Gly Gln Glu Leu Ala
 70 180 185 190

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72 Pro Gly Val Val Ser Arg Met Asp Gly Val Gly Ser Leu Pro Leu Pro
73      195      200      205
75 Arg Arg Val Arg Val Asp Tyr Leu Arg Lys Glu Arg Ala Ala Leu Arg
76      210      215      220
78 Ile Pro Leu Ser Ala Trp Val Glu Lys Glu Pro Tyr Arg Pro Gly Glu
79 225      230      235      240
81 Val Leu Ala Glu Leu Ser Glu Pro Tyr Leu Phe Arg Ala Glu Glu Ser
82      245      250      255
84 Gly Val Val Glu Leu Lys Asp Leu Ala Glu Gly His Leu Ile Tyr Leu
85      260      265      270
87 Arg Gln Glu Glu Glu Val Val Ala Arg Tyr Phe Leu Pro Ala Gly Met
88      275      280      285
90 Thr Pro Leu Val Val Glu Gly Glu Ile Val Glu Val Gly Gln Pro Leu
91      290      295      300
93 Ala Glu Gly Lys Gly Leu Leu Arg Leu Pro Arg His Met Thr Ala Lys
94 305      310      315      320
96 Glu Val Glu Ala Glu Glu Glu Gly Asp Ser Val His Leu Thr Leu Phe
97      325      330      335
99 Leu Glu Trp Thr Glu Pro Lys Asp Tyr Lys Val Ala Pro His Met Asn
100      340      345      350
102 Val Ile Val Pro Glu Gly Ala Lys Val Gln Ala Gly Glu Lys Ile Val
103      355      360      365
105 Ala Ala Ile Asp Pro Glu Glu Glu Val Ile Ala Gln Ala Glu Gly Val
106      370      375      380
108 Val His Leu His Glu Pro Ala Ser Ile Leu Val Val Lys Ala Arg Val
109 385      390      395      400
111 Tyr Pro Phe Glu Asp Asp Val Glu Val Thr Thr Gly Asp Arg Val Ala
112      405      410      415
114 Pro Gly Asp Val Leu Ala Asp Gly Gly Lys Val Lys Ser Glu Ile Tyr
115      420      425      430
117 Gly Arg Val Glu Val Asp Leu Val Arg Asn Val Val Arg Val Val Glu
118      435      440      445
120 Ser Tyr Asp Ile Asp Ala Arg Met Gly Ala Glu Ala Ile Gln Glu Leu
121      450      455      460
123 Leu Lys Glu Leu Asp Leu Glu Lys Leu Glu Arg Glu Leu Leu Glu Glu
124 465      470      475      480
126 Met Lys His Pro Ser Arg Ala Arg Arg Ala Lys Ala Arg Lys Arg Leu
127      485      490      495
129 Glu Val Val Arg Ala Phe Leu Asp Ser Gly Asn Arg Pro Glu Trp Met
130      500      505      510
132 Ile Leu Glu Ala Val Pro Val Leu Pro Pro Asp Leu Arg Pro Met Val
133      515      520      525
135 Gln Val Asp Gly Gly Arg Phe Ala Thr Ser Asp Leu Asn Asp Leu Tyr
136      530      535      540
138 Arg Arg Leu Ile Asn Arg Asn Asn Arg Leu Lys Lys Leu Leu Ala Gln
139 545      550      555      560
141 Gly Ala Pro Glu Ile Ile Ile Arg Asn Glu Lys Arg Met Leu Gln Glu
142      565      570      575
144 Ala Val Asp Ala Val Ile Asp Asn Gly Arg Arg Gly Ser Pro Val Thr

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145		580		585		590
147	Asn	Pro	Gly	Ser	Glu	Arg
148		595		600		605
150	Gly	Lys	Gln	Gly	Arg	Phe
151		610		615		620
153	Tyr	Ser	Gly	Arg	Ser	Val
154		625		630		635
156	Gln	Cys	Gly	Leu	Pro	Lys
157			645		650	655
159	Leu	Leu	Lys	Lys	Met	Glu
160			660		665	670
162	Ala	Arg	Arg	Met	Leu	Glu
163			675		680	685
165	Asp	Ala	Leu	Glu	Glu	Val
166			690		695	700
168	Ala	Pro	Thr	Leu	His	Arg
169		705			710	715
171	Val	Glu	Gly	Gln	Ser	Ile
172			725			730
174	Asn	Ala	Asp	Phe	Asp	Gly
175			740		745	750
177	Ser	Phe	Ala	Gln	Ala	Arg
178			755		760	765
180	Leu	Leu	Ser	Pro	Ala	Ser
181			770		775	780
183	Ile	Ile	Leu	Gly	Leu	Tyr
184			785		790	795
186	Gly	Ala	Gly	Met	Ala	Phe
187				805		810
189	Glu	Arg	Gly	Glu	Val	Ala
190			820		825	830
192	Glu	Thr	Ser	Val	Gly	Arg
193			835		840	845
195	Ala	Leu	Leu	Ala	Val	Ala
196			850		855	860
198	Thr	Val	Arg	Tyr	Leu	Gly
199			865		870	875
201	Leu	Phe	Ala	Arg	Ile	Val
202				885		890
204	Gln	Glu	Leu	Ile	Gln	Met
205			900		905	910
207	Asp	Leu	Val	Tyr	Gln	Ala
208			915		920	925
210	Arg	Leu	Leu	Asp	Ala	Leu
211			930		935	940
213	Ser	Gly	Ile	Ile	Thr	Ile
214			945		950	955
216	Lys	Gln	Arg	Tyr	Leu	Glu
217				965		970

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219 Gln Ala Tyr Glu Met Gly Phe Leu Thr Asp Arg Glu Arg Tyr Asp Gln
220          980          985          990
222 Val Ile Gln Leu Trp Thr Glu Thr Thr Glu Lys Val Thr Gln Ala Val
223          995          1000          1005
225 Phe Asn Asn Phe Glu Glu Asn Tyr Pro Phe Asn Pro Leu Tyr Val Met
226          1010          1015          1020
228 Ala Gln Ser Gly Ala Arg Gly Asn Pro Gln Gln Ile Arg Gln Leu Cys
229 1025          1030          1035          1040
231 Gly Met Arg Gly Leu Met Gln Lys Pro Ser Gly Glu Thr Phe Glu Val
232          1045          1050          1055
234 Pro Val Arg Ser Ser Phe Arg Glu Gly Leu Thr Val Leu Glu Tyr Phe
235          1060          1065          1070
237 Ile Ser Ser His Gly Ala Arg Lys Gly Gly Ala Asp Thr Ala Leu Arg
238          1075          1080          1085
240 Thr Ala Asp Ser Gly Tyr Leu Thr Arg Lys Leu Val Asp Val Ala His
241          1090          1095          1100
243 Glu Ile Val Val Arg Glu Ala Asp Cys Gly Thr Thr Lys Tyr Ile Ser
244 1105          1110          1115          1120
246 Val Pro Leu Phe Gln Met Asp Glu Val Thr Arg Thr Leu Arg Leu Arg
247          1125          1130          1135
249 Lys Arg Ser Asp Ile Glu Ser Gly Leu Tyr Gly Arg Val Leu Ala Arg
250          1140          1145          1150
252 Glu Val Glu Ala Leu Gly Arg Arg Leu Glu Glu Gly Arg Tyr Leu Ser
253          1155          1160          1165
255 Leu Glu Asp Val His Phe Leu Ile Lys Ala Ala Glu Ala Gly Glu Val
256          1170          1175          1180
258 Arg Glu Val Pro Val Arg Ser Pro Leu Thr Cys Gln Thr Arg Tyr Gly
259 1185          1190          1195          1200
261 Val Cys Gln Lys Cys Tyr Gly Tyr Asp Leu Ser Met Ala Arg Pro Val
262          1205          1210          1215
264 Ser Ile Gly Glu Ala Val Gly Val Val Ala Ala Glu Ser Ile Gly Glu
265          1220          1225          1230
W--> 267 Pro Gly Thr Gln Leu Thr Met Arg Thr Phe His Thr Gly Gly Xaa Ala
268          1235          1240          1245
270 Val Gly Thr Asp Ile Thr Gln Gly Leu Pro Arg Val Ile Glu Leu Phe
271          1250          1255          1260
273 Glu Ala Arg Arg Pro Lys Ala Lys Ala Val Ile Ser Glu Ile Asp Gly
274 1265          1270          1275          1280
276 Val Val Arg Ile Glu Glu Gly Glu Asp Arg Leu Ser Val Phe Val Glu
277          1285          1290          1295
279 Ser Glu Gly Phe Ser Lys Glu Tyr Lys Leu Pro Lys Asp Ala Arg Leu
280          1300          1305          1310
282 Leu Val Lys Asp Gly Asp Tyr Val Glu Ala Gly Gln Pro Leu Thr Arg
283          1315          1320          1325
285 Gly Ala Ile Asp Pro His Gln Leu Leu Glu Ala Lys Gly Pro Glu Ala
286          1330          1335          1340
288 Val Glu Arg Tyr Leu Val Asp Glu Ile Gln Lys Val Tyr Arg Ala Gln
289 1345          1350          1355          1360
291 Gly Val Lys Leu His Asp Lys His Ile Glu Ile Val Val Arg Gln Met

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292          1365          1370          1375
294 Leu Lys Tyr Val Glu Val Thr Asp Pro Gly Asp Ser Pro Leu Leu Glu
295          1380          1385          1390
297 Gly Gln Val Leu Glu Lys Trp Asp Val Glu Ala Leu Asn Glu Arg Leu
298          1395          1400          1405
300 Ile Ala Glu Gly Lys Val Pro Val Ala Trp Lys Pro Leu Leu Met Gly
301          1410          1415          1420
303 Val Thr Lys Ser Ala Leu Ser Thr Lys Ser Trp Leu Ser Ala Ala Ser
304 1425          1430          1435          1440
306 Phe Gln Asn Thr Thr His Val Leu Thr Glu Ala Ala Ile Ala Gly Lys
307          1445          1450          1455
309 Lys Asp Glu Leu Ile Gly Leu Lys Glu Asn Val Ile Leu Gly Arg Leu
310          1460          1465          1470
312 Ile Pro Ala Gly Thr Gly Ser Asp Phe Val Arg Phe Thr Gln Val Val
313          1475          1480          1485
315 Asp Gln Arg Thr Leu Lys Ala Ile Glu Glu Ala Arg Lys Glu Ala Val
316 1490          1495          1500
318 Glu Ala Lys Glu Lys Glu Ala Pro Arg Arg Pro Val Arg Arg Glu Gln
319 1505          1510          1515          1520
321 Pro Gly Lys Gly Leu
322          1525
325 <210> SEQ ID NO: 2
326 <211> LENGTH: 1119
327 <212> TYPE: PRT
328 <213> ORGANISM: Thermus aquaticus
330 <220> FEATURE:
331 <221> NAME/KEY: SITE
332 <222> LOCATION: (695)..(696)
333 <223> OTHER INFORMATION: Any amino acids can be at these two positions.
335 <400> SEQUENCE: 2
336 Met Lys Ile Lys Arg Phe Gly Arg Ile Arg Glu Val Ile Pro Leu Pro
337 1          5          10          15
339 Pro Leu Thr Glu Ile Gln Val Glu Ser Tyr Lys Lys Ala Leu Gln Ala
340          20          25          30
342 Asp Val Pro Pro Glu Lys Arg Glu Asn Val Gly Ile Gln Ala Ala Phe
343          35          40          45
345 Lys Glu Thr Phe Pro Ile Glu Glu Gly Asp Lys Gly Lys Gly Gly Leu
346          50          55          60
348 Val Leu Asp Phe Leu Glu Tyr Arg Ile Gly Asp Pro Pro Phe Ser Gln
349 65          70          75          80
351 Asp Glu Cys Arg Glu Lys Asp Leu Thr Tyr Gln Ala Pro Leu Tyr Ala
352          85          90          95
354 Arg Leu Gln Leu Ile His Lys Asp Thr Gly Leu Ile Lys Glu Asp Glu
355          100          105          110
357 Val Phe Leu Gly His Leu Pro Leu Met Thr Glu Asp Gly Ser Phe Ile
358          115          120          125
360 Ile Asn Gly Ala Asp Arg Val Ile Val Ser Gln Ile His Arg Ser Pro
361          130          135          140
363 Gly Val Tyr Phe Thr Pro Asp Pro Ala Arg Pro Gly Arg Tyr Ile Ala

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/782,714

DATE: 03/29/2001

TIME: 09:59:33

Input Set : N:\Crf3\RULE60\09782714.txt

Output Set: N:\CRF3\03292001\I782714.raw

L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2